

Minimifield

#196

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1645

RAW SEQUENCE LISTING

PATENT APPLICATION: US/08/753,750A

DATE: 07/17/2000

TIME: 16:31:02

Input Set : A:\Seqlist.txt

Output Set: N:\CRF3\07172000\H753750A.raw

4 <110> APPLICANT: Lo, Reggie Y.C.
5 Schryvers, Anthony B.
6 Potter, Andrew A.
8 <120> TITLE OF INVENTION: TRANSFERRIN BINDING PROTEINS OF
9 PASTEURELLA HAEMOLYTICA AND VACCINES CONTAINING SAME
12 <130> FILE REFERENCE: 021645.0105
14 <140> CURRENT APPLICATION NUMBER: 08/753,750A
15 <141> CURRENT FILING DATE: 1996-11-29
17 <150> PRIOR APPLICATION NUMBER: US 60/008,569
18 <151> PRIOR FILING DATE: 1995-12-01
20 <150> PRIOR APPLICATION NUMBER: CA 2,164,274
21 <151> PRIOR FILING DATE: 1995-12-01
23 <160> NUMBER OF SEQ ID NOS: 52
25 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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28 <211> LENGTH: 2792
29 <212> TYPE: DNA /
30 <213> ORGANISM: Pasteurella haemolytica
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35 gctgttctg atgaagtatt tgtgacagag agccattatg ctcacgaacg tcaaaacgaa 180
36 gtaactggct tggggaaagt agtgaataat tatcacgaaa tgagtaaaaa tcaaatcttt 240
37 ggtattcgtg atttaactcg ctatgaccct ggtatttcgg tgggtggaaca aggtcgcggt 300
38 gcaagtagtg gctatgccat tcgagggtga gataaaaaacc gtgtcagett acttggtgat 360
39 gggctaccac aagcgcacag ttatcatacg ctagggttcag atgctaattg tggtgcaatt 420
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42 attattaaag aggggcagca ttggggctta gatagtaaga cctcttatgc cagcaaaaaa 600
43 agccattttt tacagtctat cgcagcggct ggtgaggcgg gtggttttga agcacttgtt 660
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50 tctgttttta tgaagtgttg ctatcacttc aactcgtctc attatcttgg cgcaattcta 1080
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55 tgggttgata gcattaaact cagtgcggat aaacaagata ttgaactata tagccgggcta 1380
56 catcgcttgc attgtagcga ttatcctgtg gtatagataaa attgcccgcc gactttggat 1440
57 aaatcttggt ctatgtatcg aactgagcgt aataattacc aagaaaagca tcgtgtcatt 1500
58 catttagaat ttgataaagc gctaaatgct ggtcaaggcg tatattaacca aaccacaaaa 1560
59 ctgaatttag ggttgggctt tgatcgattt aattcgctta tggatcatgg ggatagact 1620
60 gcccaatata ccaaaggcgg ttataccagc taccgcggta gagggcggtt agataatcca 1680

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TECH CENTER 11600/2800

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63 cgcgatcttag tgataagcga gtatgtggat ttgggattag ggggtgcgtt tgatcaacat 1860
64 cgatttaaat ctgatgatcc gtggacactt agccgaactt atcgaaattg gtcttggaat 1920
65 ggtgggatta cgcttaaacc aacagagttt gtatcgctt cttatcgcat ttcaaacggt 1980
66 tttagagtgc ctgcattcta tgaactttat ggtaaacgtg atcatattgg gcttaaagat 2040
67 aacgaatatg tgcaacgcgc gcaacgtagc caccagttag agccagaaaa atcgactaat 2100
68 catgagattg gagttagctt taaagggtcaa tttggttacc ttgatgtgag ctatttccgt 2160
69 aataactata aaaatatgat tgcgacagca tgtaaaagaa taatacaaaa atcacactgt 2220
70 ttctataact accataatat tcaagatgta gcactaaacg ggataaattt agtcgctaaa 2280
71 tttgacttac acggtatttt atctatgctg ccagatgggt tttattcatc agttgtttat 2340
72 aaccgtgtta aagtaaaaga gcggaaacta accgactcaa gactcgatag cgtaaacgat 2400
73 cctatttctag atgcgattca gccagcacgc tatgtgcttg gattcggcta cgatcaccca 2460
74 gaagaaaaat ggggaatttg cattactacc acctattcta aagccaaaaa cgccgatgag 2520
75 gtggcaggca cacgctcatc cggatacatc gcgttgattt aggtggcaaa ctgaccggtt 2580
76 cttgtgtcac ccatgatatt accggttaca tcaattataa aaactacacc ttacgtggag 2640
77 gaatttataa tgtgactaat cgtaaatatt ccacttggga atcagtgcgc caatccggtg 2700
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82 <211> LENGTH: 930
83 <212> TYPE: PRT
84 <213> ORGANISM: Pasteurella haemolytica
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90 20 25 30
91 Lys Ile Glu Glu Asn Asn Asp Leu Ala Val Leu Asp Glu Val Ile Val
92 35 40 45
93 Thr Glu Ser His Tyr Ala His Glu Arg Gln Asn Glu Val Thr Gly Leu
94 50 55 60
95 Gly Lys Val Val Lys Asn Tyr His Glu Met Ser Lys Asn Gln Ile Leu
96 65 70 75 80
97 Gly Ile Arg Asp Leu Thr Arg Tyr Asp Pro Gly Ile Ser Val Val Glu
98 85 90 95
99 Gln Gly Arg Gly Ala Ser Ser Gly Tyr Ala Ile Arg Gly Val Asp Lys
100 100 105 110
101 Asn Arg Val Ser Leu Leu Val Asp Gly Leu Pro Gln Ala His Ser Tyr
102 115 120 125
103 His Thr Leu Gly Ser Asp Ala Asn Gly Gly Ala Ile Asn Glu Ile Glu
104 130 135 140
105 Tyr Glu Asn Ile Arg Ser Ile Glu Leu Ser Lys Gly Ala Ser Ser Ala
106 145 150 155 160
107 Glu Tyr Gly Ser Gly Ala His Gly Gly Ala Ile Gly Phe Arg Thr Lys
108 165 170 175
109 Asp Ala Gln Asp Ile Ile Lys Glu Gly Gln His Trp Gly Leu Asp Ser
110 180 185 190
111 Lys Thr Ser Tyr Ala Ser Lys Asn Ser His Phe Leu Gln Ser Ile Ala

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115 Arg His Gly Lys Glu Thr Lys Ile His Ser Glu Ala Asn Lys Leu Lys
116 225          230          235          240
117 His Asn Ile Arg Arg Ile Thr Gly Phe Glu Asn Arg Tyr Asp Phe Thr
118          245          250          255
119 Gln Ile Pro His Arg Met Leu Leu Glu Asp Leu Leu Leu Ile Val Glu
120          260          265          270
121 Asp Thr Cys Pro Thr Leu Asp Cys Thr Pro Arg Ala Arg Val Lys Leu
122          275          280          285
123 Asn Arg Asp Asn Phe Pro Val Arg Thr Phe Pro Glu Tyr Thr Pro Glu
124          290          295          300
125 Glu Arg Lys Gln Leu Glu Gln Ile Pro Tyr Arg Thr Glu Gln Leu Ser
126 305          310          315          320
127 Ala Gln Glu Tyr Thr Gly Lys Asp Arg Ile Ala Pro Asn Pro Leu Asp
128          325          330          335
129 Tyr Lys Ser Asn Ser Val Phe Met Lys Phe Gly Tyr His Phe Asn Ser
130          340          345          350
131 Ser His Tyr Leu Gly Ala Ile Leu Glu Asp Thr Lys Thr Arg Tyr Asp.
132          355          360          365
133 Ile Arg Asp Met Gln Thr Pro Ala Tyr Tyr Thr Lys Asp Asp Ile Asn
134          370          375          380
135 Leu Ser Leu Arg Asn Tyr Val Tyr Glu Gly Asp Asn Ile Leu Asp Gly
136 385          390          395          400
137 Leu Val Phe Lys Pro Arg Ile Pro Tyr Gly Leu Arg Tyr Ser His Val
138          405          410          415
139 Lys Phe Phe Asp Glu Arg His His Lys Arg Arg Leu Gly Phe Thr Tyr
140          420          425          430
141 Lys Tyr Lys Pro Glu Asn Asn Arg Trp Leu Asp Ser Ile Lys Leu Ser
142          435          440          445
143 Ala Asp Lys Gln Asp Ile Glu Leu Tyr Ser Arg Leu His Arg Leu His
144          450          455          460
145 Cys Ser Asp Tyr Pro Val Val Asp Lys Asn Cys Arg Pro Thr Leu Asp
146 465          470          475          480
147 Lys Ser Trp Ser Met Tyr Arg Thr Glu Arg Asn Asn Tyr Gln Glu Lys
148          485          490          495
149 His Arg Val Ile His Leu Glu Phe Asp Lys Ala Leu Asn Ala Gly Gln
150          500          505          510
151 Gly Val Phe Asn Gln Thr His Lys Leu Asn Leu Gly Leu Gly Phe Asp
152          515          520          525
153 Arg Phe Asn Ser Leu Met Asp His Gly Asp Met Thr Ala Gln Tyr Thr
154          530          535          540
155 Lys Gly Gly Tyr Thr Ser Tyr Arg Gly Arg Gly Arg Leu Asp Asn Pro
156 545          550          555          560
157 Tyr Ile Tyr Arg Arg Asp Pro Arg Ser Ile Glu Thr Val Ser Leu Cys
158          565          570          575
159 Asn Asn Thr Arg Gly Asp Ile Leu Asn Cys Glu Pro Arg Lys Ile Lys
160          580          585          590

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161 Gly Asp Ser His Phe Val Ser Phe Arg Asp Leu Val Ile Ser Glu Tyr
162      595      600      605
163 Val Asp Leu Gly Leu Gly Val Arg Phe Asp Gln His Arg Phe Lys Ser
164      610      615      620
165 Asp Asp Pro Trp Thr Leu Ser Arg Thr Tyr Arg Asn Trp Ser Trp Asn
166 625      630      635      640
167 Gly Gly Ile Thr Leu Lys Pro Thr Glu Phe Val Ser Leu Ser Tyr Arg
168      645      650      655
169 Ile Ser Asn Gly Phe Arg Val Pro Ala Phe Tyr Glu Leu Tyr Gly Lys
170      660      665      670
171 Arg Asp His Ile Gly Leu Lys Asp Asn Glu Tyr Val Gln Arg Ala Gln
172      675      680      685
173 Arg Ser His Gln Leu Glu Pro Glu Lys Ser Thr Asn His Glu Ile Gly
174      690      695      700
175 Val Ser Phe Lys Gly Gln Phe Gly Tyr Leu Asp Val Ser Tyr Phe Arg
176 705      710      715      720
177 Asn Asn Tyr Lys Asn Met Ile Ala Thr Ala Cys Lys Arg Ile Ile Gln
178      725      730      735
179 Lys Ser His Cys Phe Tyr Asn Tyr His Asn Ile Gln Asp Val Ala Leu
180      740      745      750
181 Asn Gly Ile Asn Leu Val Ala Lys Phe Asp Leu His Gly Ile Leu Ser
182      755      760      765
183 Met Leu Pro Asp Gly Phe Tyr Ser Ser Val Ala Tyr Asn Arg Val Lys
184      770      775      780
185 Val Lys Glu Arg Lys Leu Thr Asp Ser Arg Leu Asp Ser Val Asn Asp
186 785      790      795      800
187 Pro Ile Leu Asp Ala Ile Gln Pro Ala Arg Tyr Val Leu Gly Phe Gly
188      805      810      815
189 Tyr Asp His Pro Glu Glu Lys Trp Gly Ile Gly Ile Thr Thr Tyr
190      820      825      830
191 Ser Lys Ala Lys Asn Ala Asp Glu Val Ala Gly Thr Arg His His Gly
192      835      840      845
193 Ile His Arg Val Asp Leu Gly Gly Lys Leu Thr Gly Ser Trp Tyr Thr
194      850      855      860
195 His Asp Ile Thr Gly Tyr Ile Asn Tyr Lys Asn Tyr Thr Leu Arg Gly
196 865      870      875      880
197 Gly Ile Tyr Asn Val Thr Asn Arg Lys Tyr Ser Thr Trp Glu Ser Val
198      885      890      895
199 Arg Gln Ser Gly Val Asn Ala Val Asn Gln Asp Arg Gly Ser Asn Tyr
200      900      905      910
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202      915      920      925
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207 <210> SEQ ID NO: 3
208 <211> LENGTH: 1755
209 <212> TYPE: DNA
210 <213> ORGANISM: Pasteurella haemolytica
212 <400> SEQUENCE: 3

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Input Set : A:\Seqlist.txt

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213 atgtttaaac ttaaaagtag ttttgtactg cttaatgcgg cgctacttgc tgcttggtcc 60
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215 cccaaaaagc caagtttaca agatgataat agtaacgcaa gacgtacagt aagcgcttct 180
216 gaaactgaag ctttattgca gccgggggtt ggtttttcag ccaaaattcc gcgtcgtaat 240
217 ctccttcgcg aggggaagga agatgtagcc cctattgggt atataaaaga gattactgga 300
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221 acaggtgcac atgggtatgt ttactattta ggtatagagc cgcccaaagc aatacctacc 540
222 caaaaactaa cttataaagg atattgggat ttactacct atgcggctaa ggggagagat 600
223 agtaatatatt ttctaattcc cgcaggcatc aatagtggcg ccataccgga aaatagtcac 660
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231 gggaaatgca cacatttgat tattaacaat aagcagattc cacttattgc ggaagccaca 1140
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238 gaacgcccaa tgcgtgacct ggaaggcaat ctgaaaagga atgggttttg aggcacagcc 1560
239 aaaacgggca attctggtt taatcttgat cccaaaagta cgaatggttg cacggtaggg 1620
240 catataaata ctcaatttga agggggcttt tatggcccta aggcgacgga attaggtggt 1680
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245 <211> LENGTH: 584
246 <212> TYPE: PRT /
247 <213> ORGANISM: Pasteurella haemolytica /
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253 20 25 30
254 Val Glu Ser Gln Thr Gln Thr Thr Pro Lys Lys Pro Ser Leu Gln Asp
255 35 40 45
256 Asp Asn Ser Asn Ala Arg Arg Thr Val Ser Ala Ser Glu Thr Glu Ala
257 50 55 60
258 Leu Leu Gln Pro Gly Phe Gly Phe Ser Ala Lys Ile Pro Arg Arg Asn
259 65 70 75 80
260 Leu Leu Pro Gln Gly Lys Glu Asp Val Ala Pro Ile Gly Asp Ile Lys
261 85 90 95
262 Glu Ile Thr Gly Asp Leu Pro Lys Ile Pro Tyr Glu Glu Glu Val Lys
263 100 105 110

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VERIFICATION SUMMARY
PATENT APPLICATION: US/08/753,750A
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Input Set : A:\Seqlist.txt
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